

0070777-000026SEQLIST.txt
SEQUENCE LISTING

<110> Genomine, Inc.
POSTECH FOUNDATION

<120> Novel Phytochrome-interacting protein and a use thereof

<130> OP05-1002

<150> KR10-2004-0013663
<151> 2004-02-27

<160> 26

<170> KopatentIn 1.71

<210> 1
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<400> 1
ggatccaaat gtcaggctct aggccgact 29

<210> 2
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<400> 2
ctcgagctac ttgtttgctg cagcgagttc 30

<210> 3
<211> 1455
<212> DNA
<213> Arabidopsis thaliana

<400> 3
atggagacca agaatgagaa ttctgatgtt tcacgggcag aggagttaa aagtcaggcc 60
aacgaagctt ttaaaggcca caaatactcc agtgctattg atctatatac aaaagctatt 120
gaactcaaca gcaacaacgc tgtgtattgg gcaaatacgtg catttgctca cacaaaactg 180
gaggaatatg gcagtgcaat acaggatgca tcgaaggcca ttgaagttga ttcaagatac 240
tctaagggct attacaggcg tgggtgctgcg tatcttgcca tgggaaaatt taaggatgcc 300
ttgaaggact tccaacaggt aaaaaggctt tctcctaata accctgatgc cacaagaaag 360
ctaaaggaat gtgagaaagc agtgatgaaa ctcaaatttg aagaagcaat ctctgtgcc 420
gtatctgaaa ggcgttcagt agctgagtc attgacttcc atacaataga gggtgagcca 480
caatattctg gtgctagaat tgaggagag gaagttacct tagattttgt gaaaacgatg 540
atggaggatt ttaagaacca aaaaacattg cataaacggt atgcctatca aatcgtctta 600

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cagactaggc aaatcttgct agcactgcct tctcttggtg atataagtgt tccacatggc      660
aaacatatca ctgtttgcgg tgacgttcat ggtcagttct acgatcttct caatatcttt      720
gagcttaatg gcctcccttc ggaggagaac ccatacctat ttaatggcga ctttgtggac      780
agaggctcat tctccgttga gatcatcctc actttgtttg ctttcaagtg catgtgccca      840
tcatccatat atctagccag aggaaaccat gaaagcaaga gcatgaacaa aatttatggt      900
tttgaggggtg aggttcgggtc caagttgagt gaaaaattcg tggatctctt tgctgaagtt      960
ttctgttacc tcccgttggc tcatgttata aatgggaagg tcttcgtggt acatggaggt     1020
cttttcagtg ttgacggcgt gaaactctca gacatcagag ccattgacag attctgtgag     1080
ccaccagagg aaggactaat gtgtgaacta ttgtggagtg atcctcaacc tctccctgga     1140
agaggcccaa gcaagcgagg agttggtcta tcatttggtg gagatgtgac aaagagggtt     1200
ttgcaagata acaattttaga tttgttggtc cggtcacatg aagtaaaaga tgaaggttat     1260
gaggttgaac atgacggtaa actcataact gtcttctctg cgccaaatta ctgtgatcag     1320
atgggtaata agggagcctt cattcgtttt gaagctcctg atatgaagcc aaacattggt     1380
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aggatgttca actaa                                           1455

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<210>      4
<211>      484
<212>      PRT
<213>      Arabidopsis thaliana

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<400>      4
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Lys Ser Gln Ala Asn Glu Ala Phe Lys Gly His Lys Tyr Ser Ser Ala
          20          25          30
Ile Asp Leu Tyr Thr Lys Ala Ile Glu Leu Asn Ser Asn Asn Ala Val
          35          40          45
Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly
          50          55          60
Ser Ala Ile Gln Asp Ala Ser Lys Ala Ile Glu Val Asp Ser Arg Tyr
          65          70          75          80
Ser Lys Gly Tyr Tyr Arg Arg Gly Ala Ala Tyr Leu Ala Met Gly Lys
          85          90          95
Phe Lys Asp Ala Leu Lys Asp Phe Gln Gln Val Lys Arg Leu Ser Pro
          100          105          110
Asn Asp Pro Asp Ala Thr Arg Lys Leu Lys Glu Cys Glu Lys Ala Val
          115          120          125
Met Lys Leu Lys Phe Glu Glu Ala Ile Ser Val Pro Val Ser Glu Arg
          130          135          140
Arg Ser Val Ala Glu Ser Ile Asp Phe His Thr Ile Glu Val Glu Pro
          145          150          155          160

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Gln Tyr Ser Gly Ala Arg Ile Glu Gly Glu Glu Val Thr Leu Asp Phe
 165 170 175
 Val Lys Thr Met Met Glu Asp Phe Lys Asn Gln Lys Thr Leu His Lys
 180 185 190
 Arg Tyr Ala Tyr Gln Ile Val Leu Gln Thr Arg Gln Ile Leu Leu Ala
 195 200 205
 Leu Pro Ser Leu Val Asp Ile Ser Val Pro His Gly Lys His Ile Thr
 210 215 220
 Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe
 225 230 235 240
 Glu Leu Asn Gly Leu Pro Ser Glu Glu Asn Pro Tyr Leu Phe Asn Gly
 245 250 255
 Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu
 260 265 270
 Phe Ala Phe Lys Cys Met Cys Pro Ser Ser Ile Tyr Leu Ala Arg Gly
 275 280 285
 Asn His Glu Ser Lys Ser Met Asn Lys Ile Tyr Gly Phe Glu Gly Glu
 290 295 300
 Val Arg Ser Lys Leu Ser Glu Lys Phe Val Asp Leu Phe Ala Glu Val
 305 310 315 320
 Phe Cys Tyr Leu Pro Leu Ala His Val Ile Asn Gly Lys Val Phe Val
 325 330 335
 Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile
 340 345 350
 Arg Ala Ile Asp Arg Phe Cys Glu Pro Pro Glu Glu Gly Leu Met Cys
 355 360 365
 Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
 370 375 380
 Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
 385 390 395 400
 Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
 405 410 415
 Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
 420 425 430
 Ser Ala Pro Asn Tyr Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile
 435 440 445
 Arg Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala
 450 455 460
 Val Pro His Pro Asp Val Lys Pro Met Ala Tyr Ala Asn Asn Phe Leu
 465 470 475 480
 Arg Met Phe Asn

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 5
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<210> 6
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 6
 ctcgagttag ttgaacatcc tgag 24

<210> 7
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 7
 ggatccgatg tcaggctcta ggccgact 28

<210> 8
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 8
 gctgatcagc atggtttccg gagtcggggg tagt 34

<210> 9
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 9
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<210> 10
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 10
ctcgagtcaa gagattgctt cttcaaa 27

<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 11
ggatccatgc cagtatctga aaggcgt 27

<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 12
atggagacca agaatgagaa ttct 24

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 13
ttagttgaac atcctgagaa agtt 24

<210> 14
<211> 347
<212> PRT
<213> Arabidopsis thaliana

<400> 14
Ser Val Pro Val Ser Glu Arg Arg Ser Val Ala Glu Ser Ile Asp Phe
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His Thr Ile Glu Val Glu Pro Gln Tyr Ser Gly Ala Arg Ile Glu Gly
20 25 30
Glu Glu Val Thr Leu Asp Phe Val Lys Thr Met Met Glu Asp Phe Lys
35 40 45
Asn Gln Lys Thr Leu His Lys Arg Tyr Ala Tyr Gln Ile Val Leu Gln
50 55 60
Thr Arg Gln Ile Leu Leu Ala Leu Pro Ser Leu Val Asp Ile Ser Val
65 70 75 80
Pro His Gly Lys His Ile Thr Val Cys Gly Asp Val His Gly Gln Phe
85 90 95

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Tyr Asp Leu Leu Asn Ile Phe Glu Leu Asn Gly Leu Pro Ser Glu Glu
 100 105 110
 Asn Pro Tyr Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser
 115 120 125
 Val Glu Ile Ile Leu Thr Leu Phe Ala Phe Lys Cys Met Cys Pro Ser
 130 135 140
 Ser Ile Tyr Leu Ala Arg Gly Asn His Glu Ser Lys Ser Met Asn Lys
 145 150 155 160
 Ile Tyr Gly Phe Glu Gly Glu Val Arg Ser Lys Leu Ser Glu Lys Phe
 165 170 175
 Val Asp Leu Phe Ala Glu Val Phe Cys Tyr Leu Pro Leu Ala His Val
 180 185 190
 Ile Asn Gly Lys Val Phe Val Val His Gly Gly Leu Phe Ser Val Asp
 195 200 205
 Gly Val Lys Leu Ser Asp Ile Arg Ala Ile Asp Arg Phe Cys Glu Pro
 210 215 220
 Pro Glu Glu Gly Leu Met Cys Glu Leu Leu Trp Ser Asp Pro Gln Pro
 225 230 235 240
 Leu Pro Gly Arg Gly Pro Ser Lys Arg Gly Val Gly Leu Ser Phe Gly
 245 250 255
 Gly Asp Val Thr Lys Arg Phe Leu Gln Asp Asn Asn Leu Asp Leu Leu
 260 265 270
 Val Arg Ser His Glu Val Lys Asp Glu Gly Tyr Glu Val Glu His Asp
 275 280 285
 Gly Lys Leu Ile Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Gln Met
 290 295 300
 Gly Asn Lys Gly Ala Phe Ile Arg Phe Glu Ala Pro Asp Met Lys Pro
 305 310 315 320
 Asn Ile Val Thr Phe Ser Ala Val Pro His Pro Asp Val Lys Pro Met
 325 330 335
 Ala Tyr Ala Asn Asn Phe Leu Arg Met Phe Asn
 340 345

<210> 15
 <211> 1041
 <212> DNA
 <213> Arabidopsis thaliana

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 gagccacaat attctggtgc tagaattgag ggagaggaag ttaccttaga ttttgtgaaa 120
 acgatgatgg aggattttta gaaccaaata acattgcata aacggtatgc ctatcaaatac 180
 gtcttacaga ctaggcaaat cttgctagca ctgcccttctc ttgttgatat aagtgttcca 240
 catggcaaac atatcactgt ttgcggtgac gttcatggtc agttctacga tcttctcaat 300
 atctttgagc ttaatggcct cccttcggag gagaacccat acctatttaa tggcgacttt 360

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gtggacagag gctcattctc cgttgagatc atcctcactt tgtttgcttt caagtgcattg      420
tgcccatcat ccatatatct agccagagga aaccatgaaa gcaagagcat gaacaaaatt      480
tatggttttg aggggtgaggt tcgggtccaag ttgagtgaaa aattcgtgga tctctttgct      540
gaagttttct gttacctccc gttgggtcat gttataaatg ggaaggtctt cgtgggtacat      600
ggaggtcttt tcagtgttga cggcgtgaaa ctctcagaca tcagagccat tgacagattc      660
tgtgagccac cagaggaagg actaatgtgt gaactattgt ggagtgatcc tcaacctctc      720
cctggaagag gccaagcaa gcgaggagtt ggtctatcat ttgggtggaga tgtgacaaag      780
aggtttttgc aagataacaa tttagatttg ttgggtccggt cacatgaagt aaaagatgaa      840
ggttatgagg ttgaacatga cggtaaactc ataactgtct tctctgcgcc aaattactgt      900
gatcagatgg gtaataaggg agccttcatt cgttttgaag ctctgatata gaagccaaac      960
attgttacat tctcagcagt gcctcatccg gatgtgaagc ctatggcata tgcaaacaac     1020
tttctcagga tgttcaacta a                                           1041

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<210>      16
<211>      479
<212>      PRT
<213>      Homo sapiens

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<220>
<221>      PEPTIDE
<222>      (1)
<223>      PAPP5

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<400>      16
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  1          5          10          15
Lys Ser Gln Ala Asn Glu Ala Phe Lys Gly His Lys Tyr Ser Ser Ala
          20          25          30
Ile Asp Leu Tyr Thr Lys Ala Ile Glu Leu Asn Ser Asn Asn Ala Val
          35          40          45
Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly
          50          55          60
Ser Ala Ile Gln Asp Ala Ser Lys Ala Ile Glu Val Asp Ser Arg Tyr
          65          70          75          80
Ser Lys Gly Tyr Tyr Arg Arg Gly Ala Ala Tyr Leu Ala Met Gly Lys
          85          90          95
Glu Lys Asp Ala Leu Lys Asp Phe Gln Gln Val Lys Gly Leu Ser Pro
          100          105          110
Asn Asp Pro Asp Ala Thr Arg Lys Leu Lys Glu Cys Glu Lys Ala Val
          115          120          125
Met Lys Leu Lys Phe Glu Glu Ala Ile Ser Val Pro Val Ser Glu Arg
          130          135          140
Arg Ser Val Ala Glu Ser Ile Asp Phe His Thr Ile Glu Val Glu Pro
          145          150          155          160
Gln Tyr Ser Gly Ala Arg Ile Glu Gly Glu Glu Val Thr Leu Asp Phe

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165

170

175

Val Lys Thr Met Met Glu Asp Phe Lys Asn Gln Lys Thr Leu His Lys
 180 185 190
 Arg Tyr Ala Tyr Gln Ile Val Leu Gln Thr Arg Gln Ile Leu Leu Ala
 195 200 205
 Leu Pro Ser Leu Val Asp Ile Ser Val Pro His Gly Lys His Ile Thr
 210 215 220
 Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe
 225 230 235 240
 Glu Asp Asn Gly Leu Pro Ser Glu Glu Asn Pro Tyr Leu Phe Asn Gly
 245 250 255
 Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu
 260 265 270
 Phe Ala Glu Lys Cys Met Cys Pro Ser Ser Ile Tyr Leu Ala Arg Gly
 275 280 285
 Asn His Glu Ser Lys Ser Met Asn Lys Ile Tyr Gly Phe Glu Gly Glu
 290 295 300
 Val Arg Ser Lys Leu Ser Glu Lys Phe Val Asp Leu Phe Ala Glu Val
 305 310 315 320
 Phe Cys Tyr Leu Pro Leu Ala His Val Ile Asn Gly Lys Val Phe Val
 325 330 335
 Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile
 340 345 350
 Arg Ala Ile Asp Arg Phe Cys Glu Pro Phe Glu Glu Gly Leu Met Cys
 355 360 365
 Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
 370 375 380
 Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
 385 390 395 400
 Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
 405 410 415
 Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
 420 425 430
 Ser Ala Pro Asn Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile Arg
 435 440 445
 Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala Val
 450 455 460
 Pro His Pro Met Ala Tyr Ala Asn Asn Phe Ile Arg Met Phe Asn
 465 470 475

<210> 17
 <211> 492
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)

<223> PP5

<400> 17
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 Gly Ala Leu Lys Arg Ala Glu Glu Leu Lys Thr Gln Ala Asn Asp Tyr
 20 25 30
 Phe Lys Ala Lys Asp Tyr Glu Asn Ala Ile Lys Phe Tyr Ser Gln Ala
 35 40 45
 Ile Glu Leu Asn Pro Ser Asn Ala Ile Tyr Tyr Gly Asn Arg Ser Leu
 50 55 60
 Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr Ala Leu Gly Asp Ala Thr
 65 70 75 80
 Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile Lys Gly Tyr Tyr Arg Arg
 85 90 95
 Ala Ala Ser Asn Met Ala Leu Gly Lys Phe Arg Ala Ala Leu Arg Asp
 100 105 110
 Tyr Glu Thr Val Val Lys Val Lys Pro His Asp Lys Asp Ala Lys Met
 115 120 125
 Lys Tyr Gln Glu Cys Asn Lys Thr Val Lys Gln Lys Ala Phe Glu Arg
 130 135 140
 Ala Ile Gly Asp Glu His Lys Arg Ser Val Val Asp Ser Leu Asp Ile
 145 150 155 160
 Glu Ser Met Thr Ile Glu Asp Glu Tyr Ser Gly Pro Lys Leu Glu Asp
 165 170 175
 Gly Lys Val Thr Ile Ser Phe Met Lys Glu Leu Met Gln Trp Tyr Lys
 180 185 190
 Asp Gln Lys Lys Leu His Arg Lys Cys Ala Tyr Gln Ile Leu Val Gln
 195 200 205
 Val Lys Glu Val Leu Ser Lys Leu Ser Thr Leu Val Glu Thr Thr Leu
 210 215 220
 Lys Glu Thr Glu Lys Ile Thr Val Cys Gly Asp Thr His Gly Gln Phe
 225 230 235 240
 Tyr Asp Leu Leu Asn Ile Phe Glu Leu Asn Gly Leu Pro Ser Glu Thr
 245 250 255
 Asn Pro Tyr Asp Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser
 260 265 270
 Val Glu Val Ile Leu Thr Leu Phe Gly Phe Lys Leu Leu Tyr Pro Asp
 275 280 285
 His Phe His Leu Leu Arg Gly Asn His Glu Thr Asp Asn Met Asn Gln
 290 295 300
 Ile Tyr Gly Phe Glu Gly Glu Val Lys Ala Lys Tyr Thr Ala Gln Met
 305 310 315 320
 Tyr Glu Leu Phe Ser Glu Val Phe Glu Trp Leu Pro Leu Ala Gln Cys
 325 330 335
 Ile Asn Gly Lys Val Leu Ile Met His Gly Gly Leu Phe Ser Glu Asp

340

345

350

Gly Val Thr Leu Asp Asp Ile Arg Lys Ile Glu Arg Asn Arg Gln Pro
 355 360 365
 Phe Asp Ser Gly Pro Met Cys Asp Leu Leu Trp Ser Asp Pro Gln Pro
 370 375 380
 Gln Asn Gly Arg Ser Ile Ser Lys Arg Gly Val Ser Cys Gln Phe Gly
 385 390 395 400
 Pro Asp Val Thr Lys Ala Phe Leu Glu Glu Asn Asn Leu Asp Tyr Ile
 405 410 415
 Ile Arg Ser His Glu Val Lys Ala Glu Gly Tyr Glu Val Ala His Gly
 420 425 430
 Gly Arg Cys Val Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Gln Met
 435 440 445
 Gly Asn Lys Ala Ser Tyr Ile His Leu Gln Gly Ser Asp Leu Arg Pro
 450 455 460
 Gln Phe His Gln Phe Thr Ala Val Pro His Pro Asn Val Lys Pro Met
 465 470 475 480
 Ala Tyr Ala Asn Thr Leu Leu Gln Leu Gly Met Met
 485 490

<210> 18
 <211> 500
 <212> PRT
 <213> Mus musculus

 <220>
 <221> PEPTIDE
 <222> (1)
 <223> PP5

<400> 18
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 1 5 10 15
 Asp Glu Pro Pro Ala Asp Gly Leu Ala Lys Arg Ala Glu Glu Leu Lys
 20 25 30
 Thr Gln Ala Asn Asp Tyr Phe Lys Ala Lys Asp Tyr Glu Asn Ala Ile
 35 40 45
 Lys Phe Tyr Ser Gln Ala Ile Glu Leu Asn Pro Gly Asn Ala Ile Tyr
 50 55 60
 Tyr Gly Asn Arg Ser Leu Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr
 65 70 75 80
 Ala Leu Gly Asp Ala Thr Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile
 85 90 95
 Lys Gly Tyr Tyr Arg Arg Ala Ala Ser Asn Met Ala Leu Gly Lys Phe
 100 105 110
 Arg Ala Ala Leu Arg Asp Tyr Glu Thr Val Val Lys Val Lys Pro Asn
 115 120 125
 Asp Lys Asp Ala Lys Met Lys Tyr Gln Glu Cys Ser Lys Thr Val Lys
 130 135 140

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Gln Lys Ala Phe Glu Arg Ala Ile Ala Gly Asp Glu His Arg Arg Ser
 145 150 155 160
 Val Val Asp Ser Leu Asp Ile Glu Ser Met Thr Ile Glu Asp Glu Tyr
 165 170 175
 Ser Gly Pro Lys Leu Glu Asp Gly Lys Val Thr Ile Thr Phe Met Lys
 180 185 190
 Asp Leu Met Gln Trp Tyr Lys Asp Gln Lys Lys Leu His Arg Lys Cys
 195 200 205
 Ala Tyr Gln Ile Leu Val Gln Val Lys Glu Val Leu Cys Lys Leu Ser
 210 215 220
 Thr Leu Val Glu Thr Thr Leu Lys Glu Thr Glu Lys Ile Thr Val Cys
 225 230 235 240
 Gly Asp Thr His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe Glu Leu
 245 250 255
 Asn Gly Leu Pro Ser Glu Thr Thr Asn Pro Tyr Thr Phe Asn Gly Asp
 260 265 270
 Phe Val Asp Arg Gly Ser Phe Ser Val Glu Val Ile Leu Thr Leu Phe
 275 280 285
 Gly Phe Lys Leu Leu Tyr Pro Asp His Phe His Leu Leu Arg Gly Asn
 290 295 300
 His Glu Thr Asp Asn Met Asn Gln Ile Tyr Gly Phe Glu Gly Glu Val
 305 310 315 320
 Lys Ala Lys Tyr Thr Ala Gln Met Tyr Glu Leu Phe Ser Glu Val Glu
 325 330 335
 Glu Trp Leu Pro Leu Ala Gln Cys Ile Asn Gly Lys Val Leu Ile Met
 340 345 350
 His Gly Gly Leu Phe Ser Glu Asp Gly Val Thr Leu Asp Asp Ile Arg
 355 360 365
 Lys Ile Glu Arg Asn Arg Gln Pro Pro Asp Ser Gly Pro Met Cys Asp
 370 375 380
 Leu Leu Trp Ser Asp Pro Gln Pro Gln Asn Gly Arg Ser Val Ser Lys
 385 390 395 400
 Arg Gly Val Ser Cys Gln Phe Gly Pro Asp Val Thr Lys Ala Phe Leu
 405 410 415
 Glu Glu Asn Gln Leu Asp Tyr Ile Ile Arg Ser His Glu Val Lys Ala
 420 425 430
 Glu Gly Tyr Glu Val Ala His Gly Gly Arg Cys Val Thr Val Phe Ser
 435 440 445
 Ala Pro Asn Tyr Cys Asp Gln Met Gly Asn Lys Ala Ser Tyr Ile His
 450 455 460
 Leu Gln Gly Ser Asp Leu Arg Pro Gln Phe His Gln Phe Thr Ala Val
 465 470 475 480
 Pro His Pro Asn Val Lys Pro Met Ala Tyr Ala Asn Thr Leu Leu Gln
 485 490 495
 Leu Gly Met Met

500

<210> 19
 <211> 497
 <212> PRT
 <213> Rattus norvegicus

<220>
 <221> PEPTIDE
 <222> (1)
 <223> PP5

<400> 19
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 Asp Asp Pro Pro Ala Glu Gly Thr Leu Lys Arg Ala Glu Glu Leu Lys
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 35 40 45
 Lys Phe Tyr Ser Gln Ala Ile Glu Leu Asn Pro Ser Asn Ala Ile Tyr
 50 55 60
 Tyr Gly Asn Arg Ser Leu Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr
 65 70 75 80
 Ala Leu Gly Asp Ala Thr Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile
 85 90 95
 Lys Gly Tyr Tyr Arg Arg Ala Ala Ser Asn Met Ala Leu Gly Lys Phe
 100 105 110
 Arg Ala Ala Leu Arg Asp Tyr Glu Thr Val Val Lys Pro Asn Asp Lys
 115 120 125
 Asp Ala Lys Met Lys Tyr Gln Glu Cys Ser Lys Thr Val Lys Gln Lys
 130 135 140
 Gln Phe Glu Arg Ala Ile Ala Gly Asp Glu His Arg Arg Ser Val Val
 145 150 155 160
 Asp Ser Leu Asp Ile Glu Ser Met Thr Leu Glu Asp Glu Tyr Ser Gly
 165 170 175
 Pro Lys Leu Glu Asp Gly Lys Val Thr Ile Thr Phe Met Lys Asp Leu
 180 185 190
 Met Gln Trp Tyr Lys Asp Gln Lys Lys Leu His Arg Lys Cys Ala Tyr
 195 200 205
 Gln Ile Leu Val Gln Val Lys Glu Val Leu Val Lys Leu Ser Thr Leu
 210 215 220
 Val Glu Thr Thr Leu Lys Glu Thr Glu Lys Ile Thr Val Cys Gly Asp
 225 230 235 240
 Thr His Gly Gln Phe Tyr Asp Leu Leu Asn Glu Phe Glu Leu Asn Gly
 245 250 255
 Leu Pro Ser Glu Thr Asn Pro Tyr Ile Glu Asn Gly Asp Phe Val Asp
 260 265 270
 Arg Gly Ser Phe Ser Val Glu Val Ile Leu Thr Leu Phe Gly Phe Lys
 275 280 285

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Leu Leu Tyr Pro Asp His Phe His Leu Leu Arg Gly Asn His Glu Thr
 290 295 300
 Asp Asn Met Asn Gln Ile Tyr Gly Phe Glu Gly Glu Val Lys Ala Lys
 305 310 315 320
 Tyr Thr Ala Gln Met Tyr Glu Leu Phe Ser Glu Val Glu Glu Trp Leu
 325 330 335
 Pro Leu Ala Gln Cys Ile Asn Gly Lys Val Leu Ile Met His Gly Gly
 340 345 350
 Leu Phe Ser Glu Asp Gly Val Thr Leu Asp Asp Ile Pro Lys Ile Glu
 355 360 365
 Arg Asn Arg Gln Pro Phe Asp Ser Gly Pro Met Cys Asp Leu Leu Trp
 370 375 380
 Ser Asp Pro Gln Pro Gln Asn Gly Arg Ser Val Ser Lys Arg Gly Val
 385 390 395 400
 Ser Cys Gln Phe Gly Pro Asp Val Thr Lys Ala Phe Leu Glu Glu Asn
 405 410 415
 Gln Leu Asp Tyr Ile Ile Arg Ser His Glu Val Lys Ala Glu Gly Tyr
 420 425 430
 Glu Val Ala His Gly Gly Arg Cys Val Thr Val Phe Ser Ala Pro Asn
 435 440 445
 Tyr Cys Asp Gln Met Gly Asn Lys Ala Ser Tyr Ile His Leu Gln Gly
 450 455 460
 Ser Asp Leu Arg Pro Gln Phe His Gln Phe Thr Ala Val Pro His Pro
 465 470 475 480
 Asn Val Lys Pro Met Ala Tyr Ala Asn Ile Leu Leu Gln Leu Gly Met
 485 490 495

Met

<210> 20
 <211> 513
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <221> PEPTIDE
 <222> (1)
 <223> PP5

<400> 20
 Met Ser Thr Pro Thr Ala Ala Asp Arg Ala Lys Ala Leu Glu Arg Lys
 1 5 10 15
 Asn Glu Gly Asn Val Phe Val Lys Glu Lys His Phe Leu Lys Ala Ile
 20 25 30
 Glu Lys Tyr Thr Glu Ala Ile Asp Leu Asp Ser Thr Gln Ser Ile Tyr
 35 40 45
 Phe Ser Asn Arg Ala Phe Ala His Phe Lys Val Asp Asn Phe Gln Ser
 50 55 60

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Ala 65 Leu Asn Asp Cys Asp 70 Glu Ala Ile Lys Leu 75 Asp Pro Lys Asn Ile 80
 Lys Ala Tyr His Arg 85 Arg Ala Leu Ser Cys 90 Met Ala Leu Leu Glu 95 Glu
 Lys Lys Ala Arg 100 Lys Asp Leu Asn Val 105 Leu Leu Lys Ala Lys 110 Pro Asn
 Asp Pro Ala 115 Ala Thr Lys Ala Leu 120 Leu Thr Cys Asp Arg 125 Phe Ile Arg
 Glu 130 Glu Arg Phe Arg Lys Ala 135 Ile Gly Gly Ala Glu 140 Asn Glu Ala Lys
 Ile 145 Ser Leu Cys Gln Thr 150 Leu Asn Leu Ser Ser 155 Phe Asp Ala Asn Ala 160
 Asp Leu Ala Asn Tyr 165 Glu Gly Pro Lys Leu 170 Glu Phe Glu Gln Leu Tyr 175
 Asp Asp Lys Asn 180 Ala Phe Lys Gly Ala 185 Lys Ile Lys Asn Met 190 Ser Gln
 Glu Phe Ile 195 Ser Lys Met Val Asn 200 Asp Leu Phe Leu Lys 205 Gly Lys Tyr
 Leu Pro 210 Lys Lys Tyr Val Ala 215 Ala Ile Thr Ser His 220 Ala Asp Thr Leu
 Phe 225 Arg Gln Glu Pro Ser 230 Met Val Glu Leu Glu 235 Asn Asn Ser Thr Pro 240
 Asp Val Lys Ile Ser 245 Val Cys Gly Asp Thr 250 His Gly Gln Phe Tyr 255 Asp
 Val Leu Asn Leu 260 Phe Arg Lys Phe Gly 265 Lys Val Gly Pro Lys 270 His Thr
 Tyr Leu Phe 275 Asn Gly Asp Phe Val 280 Asp Arg Gly Ser Trp 285 Ser Cys Glu
 Val Ala 290 Leu Leu Phe Tyr Cys 295 Leu Lys Ile Leu His 300 Pro Asn Asn Phe
 Phe 305 Leu Asn Arg Gly Asn 310 His Glu Ser Asp Asn 315 Met Asn Lys Ile Tyr 320
 Gly Phe Glu Asp Glu 325 Cys Lys Tyr Lys Tyr 330 Ser Gln Arg Thr Phe 335 Asn
 Met Phe Ala Gln 340 Ser Phe Glu Ser Leu 345 Pro Leu Ala Thr Leu 350 Ile Asn
 Asn Asp Tyr 355 Leu Val Met His Gly 360 Gly Leu Pro Ser Asp 365 Pro Ser Ala
 Thr Leu 370 Ser Asp Phe Lys Asn 375 Ile Asp Arg Phe Ala 380 Gln Pro Pro Arg
 Asp 385 Gly Ala Phe Met Glu 390 Leu Leu Trp Ala Asp 395 Pro Gln Glu Ala Asn 400
 Gly Met Gly Pro Ser 405 Gln Arg Gly Leu Gly 410 His Ala Phe Gly Pro 415 Asp
 Ile Thr Asp Arg 420 Phe Leu Arg Asn Asn 425 Lys Leu Arg Lys Ile 430 Phe Arg

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Ser His Glu Leu Arg Met Gly Gly Val Gln Phe Glu Gln Lys Gly Lys
435 440 445
Leu Met Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Ser Gln Gly Asn
450 455 460
Leu Gly Gly Val Ile His Val Val Pro Gly His Gly Ile Leu Gln Ala
465 470 475 480
Gly Arg Asn Asp Asp Gln Asn Leu Ile Ile Glu Thr Phe Glu Ala Val
485 490 495
Glu His Pro Asp Ile Lys Pro Met Ala Tyr Ser Asn Gly Gly Phe Gly
500 505 510
Leu

<210> 21
<211> 520
<212> PRT
<213> Drosophila melanogaster

<220>
<221> PEPTIDE
<222> (1)
<223> PP5

<400> 21
Met Ser Ser Ser Glu Leu Glu Val Gln Lys Ala Ala Asp Cys Gln Gln
1 5 10 15
Glu Ala Lys Val Pro Ala Ser Val Glu Ile Thr Gly Ser Lys Gln Pro
20 25 30
Glu Glu Asp Thr Asn Ala Arg Thr Lys Ala Glu Leu Asp Phe Ala Ala
35 40 45
Ala Glu Gln Tyr Lys Asn Gln Gly Asn Glu Met Leu Lys Thr Lys Glu
50 55 60
Phe Ser Lys Ala Ile Asp Met Tyr Thr Lys Ala Leu Glu Leu His Pro
65 70 75 80
Asn Ser Ala Ile Tyr Tyr Ala Asn Arg Ser Leu Ala His Leu Arg Gln
85 90 95
Glu Ser Phe Gly Phe Ala Leu Gln Asp Gly Val Ser Ala Val Lys Ala
100 105 110
Asp Pro Ala Tyr Leu Lys Gly Tyr Tyr Arg Arg Ala Ala Ala His Met
115 120 125
Ser Leu Gly Lys Phe Lys Gln Ala Leu Cys Asp Phe Glu Phe Val Ala
130 135 140
Lys Cys Arg Pro Asn Asp Lys Asp Ala Lys Ile Lys Phe Thr Glu Cys
145 150 155 160
Asn Lys Thr Val Lys Met Arg Ala Phe Glu Arg Ala Ile Ala Val Asp
165 170 175
Lys Pro Glu Lys Thr Leu Ser Glu Met Tyr Ser Asp Met Glu Asn Ile
180 185 190

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Thr Ile Glu Asp Asp Tyr Lys Gly Pro Gln Leu Glu Asp Gly Lys Val
195 200 205

Thr Leu Lys Phe Met Lys Glu Leu Met Glu His Thr Lys Ala Gln Lys
210 215 220

Arg Leu His Arg Lys Phe Ala Tyr Lys Ile Leu Cys Glu Ile Asp Thr
225 230 235 240

Tyr Met Arg Ala Gln Pro Ser Leu Val Asp Ile Thr Val Pro Asp Glu
245 250 255

Glu Lys Glu Thr Ile Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu
260 265 270

Met Asn Ile Phe Glu Ile Asn Gly Leu Pro Ser Glu Lys Asn Pro Tyr
275 280 285

Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Cys
290 295 300

Ile Glu Thr Leu Phe Gly Phe Lys Leu Leu Tyr Pro Asn His Phe Phe
305 310 315 320

Leu Ala Arg Gly Asn His Glu Ser Ile Asn Met Asn Gln Met Tyr Gly
325 330 335

Glu Thr Gly Glu Val Thr Ala Lys Tyr Thr Ser Ala Met Ala Asp Ile
340 345 350

Phe Thr Gln Val Glu Asn Trp Leu Pro Leu Cys His Cys Ile Asn Gln
355 360 365

Lys Ile Leu Val Met His Gly Gly Leu Phe Ser Thr Glu Asp Val Thr
370 375 380

Leu Asp His Ile Arg Arg Ile Glu Arg Asn Cys Gln Pro Pro Glu Glu
385 390 395 400

Gly Leu Met Cys Glu Leu Leu Trp Ser Asp Pro Gln Gln Trp Met Gly
405 410 415

Leu Gly Gln Ser Lys Arg Gly Val Gly Ile Gln Phe Gly Pro Asp Val
420 425 430

Thr Glu Lys Glu Cys Lys Asp Asn Asn Leu Asp Tyr Ile Ile Arg Ser
435 440 445

His Glu Val Lys Asp Met Gly Tyr Glu Val Ala His Asn Gly Lys Cys
450 455 460

Ile Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Thr Met Gly Asn Met
465 470 475 480

Gly Ala Phe Ile Thr Ile Thr Gly Asn Asn Leu Lys Pro Asn Tyr Lys
485 490 495

Ser Phe Glu Ala Val Pro His Pro Asp Val Lys Pro Met Ala Tyr Ala
500 505 510

Asn Ser Leu Met Asn Trp Leu Ala
515 520

<210> 22
<211> 524
<212> PRT
<213> Caenorhabditis elegans

<220>
 <221> PEPTIDE
 <222> (1)
 <223> PP5

<400> 22
 Met Ala Ala Thr Ile Thr Asp Asp Ile Val Ala Thr Val Leu Glu Ser
 1 5 10 15
 Ile Glu Glu Lys Ser Tyr Glu Asp Glu Lys Glu Lys Ala Gly Met Ile
 20 25 30
 Lys Asp Glu Ala Asn Gln Phe Phe Lys Asp Gln Val Tyr Asp Val Ala
 35 40 45
 Ala Asp Leu Tyr Ser Val Ala Ile Glu Ile His Pro Thr Ala Val Leu
 50 55 60
 Tyr Gly Asn Arg Ala Gln Ala Tyr Leu Lys Lys Glu Leu Tyr Gly Ser
 65 70 75 80
 Ala Leu Asp Asp Ala Asp Asn Ala Ile Ala Ile Asp Pro Ser Tyr Val
 85 90 95
 Lys Gly Phe Tyr Arg Arg Ala Thr Ala Asn Met Ala Leu Gly Arg Phe
 100 105 110
 Lys Lys Ala Leu Thr Asp Tyr Gln Ala Val Val Lys Val Cys Pro Asn
 115 120 125
 Asp Lys Asp Ala Arg Ala Lys Phe Asp Glu Cys Ser Lys Ile Val Arg
 130 135 140
 Arg Gln Lys Phe Glu Ala Ala Ile Ser Thr Asp His Asp Lys Lys Thr
 145 150 155 160
 Val Ala Glu Thr Leu Asp Ile Asn Met Ala Ile Glu Asp Ser Tyr Asp
 165 170 175
 Gly Pro Arg Leu Glu Asp Lys Ile Thr Lys Glu Phe Val Leu Gln Leu
 180 185 190
 Ile Lys Thr Phe Lys Asn Gln Gln Lys Leu His Lys Lys Tyr Ala Phe
 195 200 205
 Lys Met Leu Leu Glu Phe Tyr Asn Tyr Val Lys Ser Leu Pro Thr Met
 210 215 220
 Val Glu Ile Thr Val Pro Thr Gly Lys Lys Phe Thr Ile Cys Gly Asp
 225 230 235 240
 Val His Gly Gln Phe Tyr Asp Leu Cys Asn Ile Phe Glu Ile Asn Gly
 245 250 255
 Tyr Pro Ser Glu Thr Asn Pro Tyr Leu Phe Asn Gly Asp Phe Val Asp
 260 265 270
 Arg Gly Ser Phe Ser Val Glu Thr Ile Phe Thr Met Ile Gly Phe Lys
 275 280 285
 Leu Leu Pro Asn His Phe Phe Met Ser Arg Gly Asn His Glu Ser Asp
 290 295 300
 Val Met Asn Lys Met Tyr Gly Phe Glu Gly Glu Val Lys Ala Lys Tyr
 305 310 315 320

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Thr Gln Gln Met Cys Asp Met Phe Thr Glu Thr Phe Cys Trp Leu Pro
325 330 335
Leu Cys His Leu Ile Asn Glu Lys Ile Phe Val Cys His Gly Gly Leu
340 345 350
Phe Lys Glu Asp Gly Val Thr Leu Glu Asp Ile Arg Lys Thr Asp Arg
355 360 365
Asn Arg Gln Pro Pro Asp Glu Gly Ile Met Cys Asp Leu Leu Trp Glu
370 375 380
Lys Asn Trp Lys Asn Leu Lys Ile Leu Tyr Pro Asp Gly Lys Ile Asn
385 390 395 400
Lys Asn Ser Asn Cys Gln Pro Lys Thr Cys Lys Asn Ala Ser Asp Pro
405 410 415
Gln Pro Ile Asn Gly Arg Ser Pro Ser Lys Arg Gly Val Gly Cys Gln
420 425 430
Phe Gly Pro Asp Val Thr Ser Lys Trp Cys Glu Thr Asn Gly Ile Glu
435 440 445
Tyr Val Val Arg Ser His Glu Val Lys Pro Glu Gly Tyr Glu Met His
450 455 460
His Asn Gly Gln Cys Phe Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp
465 470 475 480
Gln Met Asn Asn Lys Gly Ala Phe Ile Thr Ile Thr Gly Asp Asn Leu
485 490 495
Thr Pro Arg Phe Thr Pro Phe Asp Ala Val Pro His Pro Lys Leu Pro
500 505 510
Pro Met Ala Tyr Ala Asn Ser Leu Phe Gly Phe Asn
515 520

<210> 23
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> PP2A motif

<400> 23
Gly Asp Xaa His Gln Gly Gln
1 5

<210> 24
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> PP2A motif

<400> 24
Gly Asp Xaa Val Xaa Arg Gly
1 5

<210> 25
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PP2A motif

<400> 25
 Arg Gly Asn His Glu
 1 5

<210> 26
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> C-terminal consensus sequence

<400> 26
 Ser Ala Pro Asn Tyr Cys
 1 5